

## **RAW SEQUENCE LISTING**

**The Biotechnology Systems Branch of the Scientific and Technical  
Information Center (STIC) no errors detected.**

Application Serial Number: 10/518, 414  
Source: PCT  
Date Processed by STIC: 11/03/2005

# ***ENTERED***



PCT

## RAW SEQUENCE LISTING

DATE: 11/03/2005

PATENT APPLICATION: US/10/518,414

TIME: 08:22:19

Input Set : A:\Seq 1st P1031.ST25.txt

Output Set: N:\CRF4\11032005\J518414.raw

3 <110> APPLICANT: Chr. Hansen A/S  
 4 Maarten van den Brink, Johannes  
 5 Harboe, Marianne K  
 6 Petersen, Steen Guldager  
 7 Rahbek-Nielsen, Henrik  
 9 <120> TITLE OF INVENTION: IMPROVED METHOD OF PRODUCING AN ASPARTIC PROTEASE  
 POLYPEPTIDE IN  
 10 A RECOMBINANT HOST ORGANISM  
 12 <130> FILE REFERENCE: P1031US00  
 C--> 14 <140> CURRENT APPLICATION NUMBER: US/10/518,414  
 C--> 14 <141> CURRENT FILING DATE: 2004-12-17  
 14 <150> PRIOR APPLICATION NUMBER: PA 2002 0092  
 15 <151> PRIOR FILING DATE: 2002-06-17  
 17 <160> NUMBER OF SEQ ID NOS: 8  
 19 <170> SOFTWARE: PatentIn version 3.3  
 21 <210> SEQ ID NO: 1  
 22 <211> LENGTH: 323  
 23 <212> TYPE: PRT  
 24 <213> ORGANISM: Bos taurus  
 26 <400> SEQUENCE: 1  
 28 Gly Glu Val Ala Ser Val Pro Leu Thr Asn Tyr Leu Asp Ser Gln Tyr  
 29 1 5 10 15  
 32 Phe Gly Lys Ile Tyr Leu Gly Thr Pro Pro Gln Glu Phe Thr Val Leu  
 33 20 25 30  
 36 Phe Asp Thr Gly Ser Ser Asp Phe Trp Val Pro Ser Ile Tyr Cys Lys  
 37 35 40 45  
 40 Ser Asn Ala Cys Lys Asn His Gln Arg Phe Asp Pro Arg Lys Ser Ser  
 41 50 55 60  
 44 Thr Phe Gln Asn Leu Gly Lys Pro Leu Ser Ile His Tyr Gly Thr Gly  
 45 65 70 75 80  
 48 Ser Met Gln Gly Ile Leu Gly Tyr Asp Thr Val Thr Val Ser Asn Ile  
 49 85 90 95  
 52 Val Asp Ile Gln Gln Thr Val Gly Leu Ser Thr Gln Glu Pro Gly Asp  
 53 100 105 110  
 56 Val Phe Thr Tyr Ala Glu Phe Asp Gly Ile Leu Gly Met Ala Tyr Pro  
 57 115 120 125  
 60 Ser Leu Ala Ser Glu Tyr Ser Ile Pro Val Phe Asp Asn Met Met Asn  
 61 130 135 140  
 64 Arg His Leu Val Ala Gln Asp Leu Phe Ser Val Tyr Met Asp Arg Asn  
 65 145 150 155 160  
 68 Gly Gln Glu Ser Met Leu Thr Leu Gly Ala Ile Asp Pro Ser Tyr Tyr  
 69 165 170 175  
 72 Thr Gly Ser Leu His Trp Val Pro Val Thr Val Gln Gln Tyr Trp Gln  
 73 180 185 190

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```

76 Phe Thr Val Asp Ser Val Thr Ile Ser Gly Val Val Val Ala Cys Glu
77      195      200      205
80 Gly Gly Cys Gln Ala Ile Leu Asp Thr Gly Thr Ser Lys Leu Val Gly
81      210      215      220
84 Pro Ser Ser Asp Ile Leu Asn Ile Gln Gln Ala Ile Gly Ala Thr Gln
85 225      230      235      240
88 Asn Gln Tyr Gly Glu Phe Asp Ile Asp Cys Asp Asn Leu Ser Tyr Met
89      245      250      255
92 Pro Thr Val Val Phe Glu Ile Asn Gly Lys Met Tyr Pro Leu Thr Pro
93      260      265      270
96 Ser Ala Tyr Thr Ser Gln Asp Gln Gly Phe Cys Thr Ser Gly Phe Gln
97      275      280      285
100 Ser Glu Asn His Ser Gln Lys Trp Ile Leu Gly Asp Val Phe Ile Arg
101      290      295      300
104 Glu Tyr Tyr Ser Val Phe Asp Arg Ala Asn Asn Leu Val Gly Leu Ala
105 305      310      315      320
108 Lys Ala Ile

```

112 &lt;210&gt; SEQ ID NO: 2

113 &lt;211&gt; LENGTH: 1142

114 &lt;212&gt; TYPE: DNA

115 &lt;213&gt; ORGANISM: artificial

117 &lt;220&gt; FEATURE:

118 &lt;223&gt; OTHER INFORMATION: DNA fragment comprising a DNA fragment of 1138 bp designed

to

119 comprise a N-H-T glycosylation site and unique Sall and XhoI

120 sites for cloning purposes (modB-XS).

122 &lt;400&gt; SEQUENCE: 2

```

123 cggtcgaccg ctacggtgac tgacacctgg cgtgccgaga tcaactgcat cccctctac      60
125 aagggaagt ctctgcgtaa ggctctcaag gagcacggtc tgctcgagga tttcctgcag      120
127 aagcagcagt acggcatcag ctctaagtac agcggtttcg gcgagggtggc cagcgtgcct      180
129 ctactaact acctggacag ccagtacttc ggtaagatct acctggcac tccccctcag      240
131 gagttcaccg ttctgttcga tactggttcc agcgacttct gggttccctc catctactgt      300
133 aagagcaacg cttgcaagaa ccaccagcgc ttcgatacct gcaagtccag caccttccag      360
135 aaccttgcca agcccccttc catccactac ggtactggca gcatgcaggg tatccttggc      420
137 tacgacaccg ttaccgtgtc caacatcgtc gatattcagc agaccgtggg tctgagcacc      480
139 caggagcctg gcgatgtctt cacttacgcc gagttcgatg gtatcctcgg catggcttac      540
141 ccctccctgg cctctgagta ctctatccct gtgttcgaca acatgatgaa ccgccacctc      600
143 gtcgctcagg atctgttcag cgtgtacatg gaccgtaacg gtcaggagtc catgcttact      660
145 ctgggcgcca tcgatccctc ttactacacc ggttccctcc actgggttcc tgtgaccgtc      720
147 cagcagtact ggcagttcac cgtggacagc gtcactatct ccggcgtggg tgtggcttgc      780
149 gaggggtggt gtcaggccat ccttgatact ggtaccagca agctcgtcgg cccctccagc      840
151 gacatcctga acatccagca ggctatcggt gccaccagca accagtacgg cgagttcgat      900
153 atcgactgcg ataacctttc ttacatgcct actgtggttt tcgagatcaa cggtaagatg      960
155 tacccttcta ctcttctgc ttacacttcc caggatcagg gcttctgtac ctctggtttc      1020
157 cagtctgaga accacagcca gaagtggatc cttggcgatg tcttcatccg cgagtactac      1080
159 tccgtcttcg accgtgccaa caacctggtg ggtctcgcta aggccatctg atcctctaga      1140
161 gt

```

164 &lt;210&gt; SEQ ID NO: 3

165 &lt;211&gt; LENGTH: 408

166 &lt;212&gt; TYPE: DNA

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167 &lt;213&gt; ORGANISM: artificial

169 &lt;220&gt; FEATURE:

170 <223> OTHER INFORMATION: an approximately 410 bp SalI-SphII I fragment made using  
171 synthetic oligonucleotides (SEQ ID XXX-1)

173 &lt;400&gt; SEQUENCE: 3

174	cggtcgaccg ctacgggtgac tgacacctgg cgtgccgaga tcaactcgcat cccctctac	60
176	aagggcaagt ctctgcgtaa ggctctcaag gagcacggtc tgctcgagga ttctctgcag	120
178	aagcagcagt acggcatcag ctctaagtac agcggtttcg gcgaggtggc cagcgtgcct	180
180	ctcactaact acctggacag ccagtacttc ggtaagatct accttggcac tccccctcag	240
182	gagttcaccg ttctgttcga tactggttcc agcgacttct gggttccctc catctactgt	300
184	aagagcaacg cttgcaagaa ccaccagcgc ttcgatcctc gcaagtccag caccttccag	360
186	aaccttggca agcccccttc catccactac ggtactggca gcatgcag	408

189 &lt;210&gt; SEQ ID NO: 4

190 &lt;211&gt; LENGTH: 233

191 &lt;212&gt; TYPE: DNA

192 &lt;213&gt; ORGANISM: artificial

194 &lt;220&gt; FEATURE:

195 <223> OTHER INFORMATION: an approximately 220 bp SphI-BsrGI fragment made using  
synthetic

196 oligonucleotides (SEQ ID XXX-2)

198 &lt;400&gt; SEQUENCE: 4

199	gcagcatgca gggatctctt ggctacgaca ccgttaccgt gtccaacatc gtcgatattc	60
201	agcagaccgt gggctctgagc acccaggagc ctggcgatgt cttcacttac gccgagttcg	120
203	atgggtatcct cggcattggct taccctccc tggcctctga gtactctatc cctgtgttcg	180
205	acaacatgat gaaccgccac ctcgctgctc aggatctggt cagcgtgtac atg	233

208 &lt;210&gt; SEQ ID NO: 5

209 &lt;211&gt; LENGTH: 200

210 &lt;212&gt; TYPE: DNA

211 &lt;213&gt; ORGANISM: Artificial

213 &lt;220&gt; FEATURE:

214 <223> OTHER INFORMATION: an approximately 190 bp BsrGI-KpnI fragment made using  
synthetic

215 oligonucleotides (SEQ ID XXX-3)

217 &lt;400&gt; SEQUENCE: 5

218	gcgtgtacat ggaccgtaac ggtcaggagt ccatgcttac tctgggcgcc atcgatccct	60
220	cttactacac cggttccctc cactgggttc ctgtgaccgt ccagcagtac tggcagttca	120
222	ccgtggacag cgtcactatc tccggcgtgg ttgtggcttg cgagggtggc tgtcaggcca	180
224	tccttgatac tggtagcagc	200

227 &lt;210&gt; SEQ ID NO: 6

228 &lt;211&gt; LENGTH: 334

229 &lt;212&gt; TYPE: DNA

230 &lt;213&gt; ORGANISM: artificial

232 &lt;220&gt; FEATURE:

233 <223> OTHER INFORMATION: an approximately 320 bp KpnI-XbaI fragment made using  
synthetic

234 oligonucleotides (SEQ ID XXX-4)

236 &lt;400&gt; SEQUENCE: 6

237	ctggtaccag caagctcgtc ggccccctcca gcgacatcct gaacatccag caggctatcg	60
239	gtgccacca gaaccagtac ggcgagttcg atatcgactg cgataacctt tcttacatgc	120
241	ctactgtggt ttctgagatc aacggtaaga tgtacccctt tactccttct gcttacactt	180
243	cccaggatca gggtcttctgt acctctggtt tccagtctga gaaccacagc cagaagtggg	240
245	tccttggcga tgtcttcatc cgcgagtact actccgtctt cgaccgtgcc aacaacctgg	300

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247 tgggtctcgc taaggccatc tgatcctcta gagt 334

250 <210> SEQ ID NO: 7

251 <211> LENGTH: 334

252 <212> TYPE: DNA

253 <213> ORGANISM: artificial

255 <220> FEATURE:

256 <223> OTHER INFORMATION: a modified KpnI-XbaI fragment designed for construction of  
the

257 modBM gene (SEQ ID XXX-5).

259 <400> SEQUENCE: 7

260 ctggtaccag caagctcgtc ggcccctcca gcgacatcct gaacatccag caggctatcg 60

262 gtgccaccca gaaccagtac ggcgagttcg atatcgactg cgataacctt tcttacatgc 120

264 ctactgtggt ttctcgagatc aacggtaaga tgtacccctt tactccttct gcttacactt 180

266 cccaggatca gggcttctgt acctctggtt tccagtctga gaaccacacc cagaagtgga 240

268 tccttggcga tgtcttcac cgcgagtact actccgtctt cgaccgtgcc aacaacctgg 300

270 tgggtctcgc taaggccatc tgatcctcta gagt 334

273 <210> SEQ ID NO: 8

274 <211> LENGTH: 66

275 <212> TYPE: DNA

276 <213> ORGANISM: artificial

278 <220> FEATURE:

279 <223> OTHER INFORMATION: synthetic polylinker (SalI-SphI-BsrGI-KpnI-XbaI) (SEQ ID  
XXX-6)

281 <400> SEQUENCE: 8

282 ggccaggcgc gccttccatg gaagaatgcg gccgctaaac catcgatggc tcgagttggc 60

284 gcgcca 66

RAW SEQUENCE LISTING ERROR SUMMARY  
PATENT APPLICATION: US/10/518,414

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Input Set : A:\Seq 1st P1031.ST25.txt  
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Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete,  
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:2,3,4,5,6,7,8

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/518,414

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Input Set : A:\Seq 1st P1031.ST25.txt

Output Set: N:\CRF4\11032005\J518414.raw

L:14 M:270 C: Current Application Number differs, Replaced Current Application No

L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date